



SEQUENCE LISTING

<110> KRIMMER, HANS-PETER
MAY, OLIVER
KLEMENT, INGO
DRAUZ, KARLHEINZ
REICHERT, DIETMAR

<120> PROCESS FOR THE PREPARATION OF ALLYSINE ACETAL

<130> 210740US0X

<140> 09/916,501

<141> 2001-07-30

<150> DE 100 37 115.9

<151> 2000-07-28

<160> 24

<170> PatentIn version 3.1

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<212> DNA

<213> *Arthrobacter aurescens*

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<213> *Arthrobacter aurescens*

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 <213> Artificial Sequence

<220>
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 <212> DNA
 <213> *Arthrobacter aurescens*

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 <211> 1263
 <212> DNA
 <213> *Arthrobacter aurescens*

<220>
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 <212> DNA
 <213> *Arthrobacter* sp.

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<210> 8

<211> 458

<212> PRT

<213> *Arthrobacter* sp.

<400> 8

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35 40 45

Gly Lys Phe Val Met Phe Gly Val Val Asp Glu His Val His Ile Ile
50 55 60

Asp Met Asp Leu Lys Asn Arg Tyr Gly Arg Phe Glu Leu Asp Ser Glu
65 70 75 80

Ser Ala Ala Val Gly Gly Ile Thr Thr Ile Ile Glu Met Pro Ile Thr
85 90 95

Phe Pro Pro Thr Thr Thr Leu Asp Ala Phe Leu Glu Lys Lys Lys Gln
100 105 110

Ala Gly Gln Arg Leu Lys Val Asp Phe Ala Leu Tyr Gly Gly Gly Val
115 120 125

Pro Gly Asn Leu Pro Glu Ile Arg Lys Met His Asp Ala Gly Ala Val
130 135 140

Gly Phe Lys Ser Met Met Ala Ala Ser Val Pro Gly Met Phe Asp Ala
145 150 155 160

Val Ser Asp Gly Glu Leu Phe Glu Ile Phe Gln Glu Ile Ala Ala Cys
165 170 175

Gly Ser Val Val Val Val His Ala Glu Asn Glu Thr Ile Ile Gln Ala
180 185 190

Leu Gln Lys Gln Ile Lys Ala Ala Gly Arg Lys Asp Met Ala Ala Tyr

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225					230					235					240
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Gly	Leu	Glu	Thr	Ser	Leu	Pro	Met	Met	Leu	Thr	Asn	Gly	Val	Asn	Lys
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Gly	Arg	Leu	Ser	Leu	Glu	Arg	Leu	Val	Glu	Val	Met	Cys	Glu	Lys	Pro
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Ala	Lys	Leu	Phe	Glu	Ile	Tyr	Pro	Gln	Lys	Gly	Thr	Leu	Gln	Val	Gly
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Ser	Asp	Ala	Asp	Leu	Leu	Ile	Leu	Asp	Leu	Asp	Ile	Asp	Thr	Lys	Val
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Asp Ala Ser Gln Phe Arg Ser Leu His Lys Tyr Ser Pro Phe Asp Gly
405 410 415

Met Pro Val Thr Gly Ala Pro Val Leu Thr Met Val Arg Gly Thr Val
420 425 430

Val Ala Glu Lys Gly Glu Val Leu Val Glu Gln Gly Phe Gly Gln Phe
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Val Thr Arg His Asp Tyr Glu Ala Ser Lys
450 455

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<211> 1377
<212> DNA
<213> *Arthrobacter* sp.

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<210> 10
 <211> 458
 <212> PRT
 <213> *Arthrobacter* sp.

<400> 10

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Ile Thr Glu Ala Asp Ile Leu Val Lys Asp Gly Lys Val Ala Ala Ile
 20 25 30

Ser Ser Asp Thr Ser Asp Val Glu Ala Ser Arg Thr Ile Asp Ala Gly
 35 40 45

Gly Lys Phe Val Met Phe Gly Val Val Asp Glu His Val His Ile Ile
 50 55 60

Asp Met Asp Leu Lys Asn Arg Tyr Gly Arg Phe Glu Leu Asp Ser Glu
 65 70 75 80

Ser Ala Ala Val Gly Gly Ile Thr Thr Ile Ile Glu Met Pro Ile Thr
 85 90 95

Phe Pro Pro Thr Thr Thr Leu Asp Ala Phe Leu Glu Lys Lys Lys Gln
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Ala Gly Gln Arg Leu Lys Val Asp Phe Ala Leu Tyr Gly Gly Gly Val
115 120 125

Pro Gly Asn Leu Pro Glu Ile Arg Lys Met His Asp Ala Gly Ala Val
130 135 140

Gly Phe Lys Ser Met Met Ala Ala Ser Ala Pro Gly Met Phe Asp Ala
145 150 155 160

Val Ser Asp Gly Glu Leu Phe Glu Ile Phe Gln Glu Ile Ala Ala Cys
165 170 175

Gly Ser Val Val Val Val His Ala Glu Asn Glu Thr Ile Ile Gln Ala
180 185 190

Leu Gln Lys Gln Ile Lys Ala Ala Gly Arg Lys Asp Met Ala Ala Tyr
195 200 205

Glu Ala Ser Gln Pro Val Phe Gln Glu Asn Glu Ala Ile Gln Arg Ala
210 215 220

Leu Leu Leu Gln Lys Glu Ala Gly Cys Arg Leu Ile Val Leu His Val
225 230 235 240

Ser Asn Pro Asp Gly Val Glu Leu Ile His Gln Ala Gln Ser Glu Gly
245 250 255

Gln Asp Val His Cys Glu Ser Gly Pro Gln Tyr Leu Asn Ile Thr Thr
260 265 270

Asp Asp Ala Glu Arg Ile Gly Pro Tyr Met Lys Val Ala Pro Pro Val
275 280 285

Arg Ser Ala Glu Met Asn Val Arg Leu Trp Glu Gln Leu Glu Asn Gly
290 295 300

Leu Ile Asp Thr Leu Gly Ser Asp His Gly Gly His Pro Val Glu Asp

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Lys	Glu	Pro	Gly	Trp	Lys	Asp	Val	Trp	Lys	Ala	Gly	Asn	Gly	Ala	Leu
				325					330					335	
Gly	Leu	Glu	Thr	Ser	Leu	Pro	Met	Met	Leu	Thr	Asn	Gly	Val	Asn	Lys
			340					345					350		
Gly	Arg	Leu	Ser	Leu	Glu	Arg	Leu	Val	Glu	Val	Met	Cys	Glu	Lys	Pro
		355					360					365			
Ala	Lys	Leu	Phe	Glu	Ile	Tyr	Pro	Gln	Lys	Gly	Thr	Leu	Gln	Val	Gly
	370					375					380				
Ser	Asp	Ala	Asp	Leu	Leu	Ile	Leu	Asp	Leu	Asp	Ile	Asp	Thr	Lys	Val
385					390					395					400
Asp	Ala	Ser	Gln	Phe	Arg	Ser	Leu	His	Lys	Tyr	Ser	Pro	Phe	Asp	Gly
				405					410					415	
Met	Pro	Val	Thr	Gly	Ala	Pro	Val	Leu	Thr	Met	Val	Arg	Gly	Thr	Val
			420					425					430		
Val	Ala	Glu	Lys	Gly	Glu	Val	Leu	Val	Glu	Gln	Gly	Phe	Gly	Gln	Phe
		435					440					445			
Val	Thr	Arg	His	Asp	Tyr	Glu	Ala	Ser	Lys						
	450					455									

<210> 11
 <211> 1377
 <212> DNA
 <213> Arthrobacter sp.

<400> 11	
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gacattctgg tgaaagacgg caaagtcgcc gcaatcagct cggacacaag tgatgttgag	120
gcgagccgaa ccattgacgc ggggtggcaag ttcgtgatgc cgggcgtggt cgatgaacat	180

gcgagccgaa ccattgacgc ggggtggcaag ttcgtgatgc cgggctgtgt cgatgaacat 240
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gccggcgcag tgggcttcaa gtcaatgatg gcagcctcag ttccggggcat gttcgacgcc 480
gtcagcgacg gcgaactggt cgaaatcttc caggagatcg cagcctgtgg ttcagtcgtc 540
gtgggtccatg ccgagaatga aacgatcatt caagcgctcc agaagcagat caaagccgct 600
ggtcgcaagg acatggccgc ctacgaggca tcccaaccag ttttccagga gaacgaggcc 660
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ggtgcaccgg ttctgacgat ggtgcgcgga acggtggtgg cagagaaggg agaagttctg 1320
gtcgagcagg gattcggcca gttcgtcacc cgtcacgact acgaggcgct gaagtga 1377

<210> 12
<211> 458
<212> PRT
<213> *Arthrobacter* sp.

<400> 12

Met Phe Asp Val Ile Val Lys Asn Cys Arg Met Val Ser Ser Asp Gly
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Ile	Thr	Glu	Ala	Asp	Ile	Leu	Val	Lys	Asp	Gly	Lys	Val	Ala	Ala	Ile	
			20					25					30			
Ser	Ser	Asp	Thr	Ser	Asp	Val	Glu	Ala	Ser	Arg	Thr	Ile	Asp	Ala	Gly	
		35					40					45				
Gly	Lys	Phe	Val	Met	Phe	Gly	Val	Val	Asp	Glu	His	Val	His	Ile	Ile	
	50					55					60					
Asp	Met	Asp	Leu	Lys	Asn	Arg	Tyr	Gly	Arg	Phe	Glu	Leu	Asp	Ser	Glu	
65					70					75					80	
Ser	Ala	Ala	Val	Gly	Gly	Ile	Thr	Thr	Ile	Ile	Glu	Met	Pro	Leu	Thr	
				85					90					95		
Phe	Pro	Pro	Thr	Thr	Thr	Leu	Asp	Ala	Phe	Leu	Glu	Lys	Lys	Lys	Gln	
			100					105					110			
Ala	Gly	Gln	Arg	Leu	Lys	Val	Asp	Phe	Ala	Leu	Tyr	Gly	Gly	Gly	Val	
		115					120					125				
Pro	Gly	Asn	Leu	Pro	Glu	Ile	Arg	Lys	Met	His	Asp	Ala	Gly	Ala	Val	
	130					135					140					
Gly	Phe	Lys	Ser	Met	Met	Ala	Ala	Ser	Val	Pro	Gly	Met	Phe	Asp	Ala	
145					150					155					160	
Val	Ser	Asp	Gly	Glu	Leu	Phe	Glu	Ile	Phe	Gln	Glu	Ile	Ala	Ala	Cys	
				165					170					175		
Gly	Ser	Val	Val	Val	Val	His	Ala	Glu	Asn	Glu	Thr	Ile	Ile	Gln	Ala	
			180					185					190			
Leu	Gln	Lys	Gln	Ile	Lys	Ala	Ala	Gly	Arg	Lys	Asp	Met	Ala	Ala	Tyr	
		195					200					205				
Glu	Ala	Ser	Gln	Pro	Val	Phe	Gln	Glu	Asn	Glu	Ala	Ile	Gln	Arg	Ala	
	210					215					220					

Leu Leu Leu Gln Lys Glu Ala Gly Cys Arg Leu Ile Val Leu His Val
 225 230 235 240

Ser Asn Pro Asp Gly Val Glu Leu Ile His Arg Ala Gln Ser Glu Gly
 245 250 255

Gln Asp Val His Cys Glu Ser Gly Pro Gln Tyr Leu Asn Ile Thr Thr
 260 265 270

Asp Asp Ala Glu Arg Ile Gly Pro Tyr Met Lys Val Ala Pro Pro Val
 275 280 285

Arg Ser Ala Glu Met Asn Val Arg Leu Trp Glu Gln Leu Glu Asn Gly
 290 295 300

Leu Ile Asp Thr Leu Gly Ser Asp His Gly Gly His Pro Val Glu Asp
 305 310 315 320

Lys Glu Pro Gly Trp Lys Asp Val Trp Lys Ala Gly Asn Gly Ala Leu
 325 330 335

Gly Leu Glu Thr Ser Leu Pro Met Met Leu Thr Asn Gly Val Asn Lys
 340 345 350

Gly Arg Leu Ser Leu Glu Arg Leu Val Glu Val Met Cys Glu Lys Pro
 355 360 365

Ala Lys Leu Phe Glu Ile Tyr Pro Gln Lys Gly Thr Leu Gln Val Gly
 370 375 380

Ser Asp Ala Asp Leu Leu Ile Leu Asp Leu Asp Ile Asp Thr Lys Val
 385 390 395 400

Asp Ala Ser Gln Phe Arg Ser Leu His Lys Tyr Ser Pro Phe Asp Gly
 405 410 415

Met Pro Val Thr Gly Ala Pro Val Leu Thr Met Val Arg Gly Thr Val

420

425

430

Val Ala Glu Lys Gly Glu Val Leu Val Glu Gln Gly Phe Gly Gln Phe
 435 440 445

Val Thr Arg His Asp Tyr Glu Ala Ser Lys
 450 455

<210> 13
 <211> 1377
 <212> DNA
 <213> *Arthrobacter* sp.

<400> 13
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 gcgagccgaa ccattgacgc ggggtggcaag ttcgtgatgc cgggcgtggc cgatgaacat 180
 gcgagccgaa ccattgacgc ggggtggcaag ttcgtgatgc cgggcgtggc cgatgaacat 240
 tctgcggccg tgggaggcat caccaccatc atcgagatgc cgataacctt cccgcccacc 300
 accacttttg acgccttcct cgaaaagaag aagcaggcgg ggcagcgggt gaaagttgac 360
 ttcgcgctct atggcggtgg agtgccggga aacctgcccg agatccgcaa aatgcacgac 420
 gccggcgcag tgggcttcaa gtcaatgatg gcagcctcag ttccgggcat gttcgacgcc 480
 gtcagcgacg gcgaactgtt cgaaatcttc caggagatcg cagcctgtgg ttcagtcgtc 540
 gtggtccatg ccgagaatga aacgatcatt caagcgctcc agaagcagat caaagccgct 600
 ggtcgcaagg acatggccgc ctacgaggca tccaaccag ttttccagga gaacgaggcc 660
 attcagcgtg cgttactact gcagaaagaa gccggctgtc gactgattgt gcttcacgtg 720
 agcaaccctg acgggggtcg gctgatacat caggcgcaat ccgagggcca ggacgtccac 780
 tgcgagtcgg gtccgcagta tctgaatatc accacggacg acgccgaacg aatcggaccg 840
 tatatgaagg tcgcgccgcc cgtccgctca gccgagatga acgccagatt atgggaacaa 900
 cttgagaacg ggctcatcga cacccttggg tcagaccacg gcggacatcc tgtcgaggac 960
 aaagaacccg gctggaagga cgtgtggaaa gccggcaacg gtgcgctggg ccttgagaca 1020

tccctgccta tgatgctgac caacggagtg aataaaggca ggctatcctt ggaacgcctc 1080
 gtcgaggtga tgtgcgagaa acctgcgaag ctctttggca tctatccgca gaagggcacg 1140
 ctacaggttg gttccgacgc cgatctgctc atcctcgatc tggatattga caccaaagtg 1200
 gatgcctcgc agttccgac cctgcataag tacagcccgt tcgacgggat gcccgtcacg 1260
 ggtgcaccgg ttctgacgat ggtgcgcgga acggtggtgg cagagaaggg agaagttctg 1320
 gtcgagcagg gattcggcca gttcgtcacc cgtcacgact acgaggcgtc gaagtga 1377

<210> 14
 <211> 458
 <212> PRT
 <213> *Arthrobacter* sp.

<400> 14

Met Phe Asp Val Ile Val Lys Asn Cys Arg Met Val Ser Ser Asp Gly
 1 5 10 15

Ile Thr Glu Ala Asp Ile Leu Val Lys Asp Gly Lys Val Ala Ala Ile
 20 25 30

Ser Ser Asp Thr Ser Asp Val Glu Ala Ser Arg Thr Ile Asp Ala Gly
 35 40 45

Gly Lys Phe Val Met Phe Gly Val Val Asp Glu His Val His Ile Ile
 50 55 60

Asp Met Asp Leu Lys Asn Arg Tyr Gly Arg Phe Glu Leu Asp Ser Glu
 65 70 75 80

Ser Ala Ala Val Gly Gly Ile Thr Thr Ile Ile Glu Met Pro Ile Thr
 85 90 95

Phe Pro Pro Thr Thr Thr Leu Asp Ala Phe Leu Glu Lys Lys Lys Gln
 100 105 110

Ala Gly Gln Arg Leu Lys Val Asp Phe Ala Leu Tyr Gly Gly Gly Val
 115 120 125

Pro	Gly	Asn	Leu	Pro	Glu	Ile	Arg	Lys	Met	His	Asp	Ala	Gly	Ala	Val	130	135	140
Gly	Phe	Lys	Ser	Met	Met	Ala	Ala	Ser	Val	Pro	Gly	Met	Phe	Asp	Ala	145	150	155
Val	Ser	Asp	Gly	Glu	Leu	Phe	Glu	Ile	Phe	Gln	Glu	Ile	Ala	Ala	Cys	165	170	175
Gly	Ser	Val	Val	Val	Val	His	Ala	Glu	Asn	Glu	Thr	Ile	Ile	Gln	Ala	180	185	190
Leu	Gln	Lys	Gln	Ile	Lys	Ala	Ala	Gly	Arg	Lys	Asp	Met	Ala	Ala	Tyr	195	200	205
Glu	Ala	Ser	Gln	Pro	Val	Phe	Gln	Glu	Asn	Glu	Ala	Ile	Gln	Arg	Ala	210	215	220
Leu	Leu	Leu	Gln	Lys	Glu	Ala	Gly	Cys	Arg	Leu	Ile	Val	Leu	His	Val	225	230	235
Ser	Asn	Pro	Asp	Gly	Val	Glu	Leu	Ile	His	Gln	Ala	Gln	Ser	Glu	Gly	245	250	255
Gln	Asp	Val	His	Cys	Glu	Ser	Gly	Pro	Gln	Tyr	Leu	Asn	Ile	Thr	Thr	260	265	270
Asp	Asp	Ala	Glu	Arg	Ile	Gly	Pro	Tyr	Met	Lys	Val	Ala	Pro	Pro	Val	275	280	285
Arg	Ser	Ala	Glu	Met	Asn	Ala	Arg	Leu	Trp	Glu	Gln	Leu	Glu	Asn	Gly	290	295	300
Leu	Ile	Asp	Thr	Leu	Gly	Ser	Asp	His	Gly	Gly	His	Pro	Val	Glu	Asp	305	310	315
Lys	Glu	Pro	Gly	Trp	Lys	Asp	Val	Trp	Lys	Ala	Gly	Asn	Gly	Ala	Leu	325	330	335

Gly Leu Glu Thr Ser Leu Pro Met Met Leu Thr Asn Gly Val Asn Lys
 340 345 350

Gly Arg Leu Ser Leu Glu Arg Leu Val Glu Val Met Cys Glu Lys Pro
 355 360 365

Ala Lys Leu Phe Glu Ile Tyr Pro Gln Lys Gly Thr Leu Gln Val Gly
 370 375 380

Ser Asp Ala Asp Leu Leu Ile Leu Asp Leu Asp Ile Asp Thr Lys Val
 385 390 395 400

Asp Ala Ser Gln Phe Arg Ser Leu His Lys Tyr Ser Pro Phe Asp Gly
 405 410 415

Met Pro Val Thr Gly Ala Pro Val Leu Thr Met Val Arg Gly Thr Val
 420 425 430

Val Ala Glu Lys Gly Glu Val Leu Val Glu Gln Gly Phe Gly Gln Phe
 435 440 445

Val Thr Arg His Asp Tyr Glu Ala Ser Lys
 450 455

<210> 15
 <211> 1377
 <212> DNA
 <213> Arthrobacter sp.

<400> 15
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 gcgagccgaa ccattgacgc ggggtggcaag ttcgtgatgc cgggcgtggt cgatgaacat 180
 gcgagccgaa ccattgacgc ggggtggcaag ttcgtgatgc cgggcgtggt cgatgaacat 240
 tctgcggccg tgggaggcat caccaccatc atcgagatgc cgttaacctt cccgcccacc 300
 accactttgg acgccttcct cgaaaagaag aagcaggcgg ggcagcggtt gaaagttgac 360

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gccggcgagcag tgggcttcaa gtcaatgatg gcagcctcag ttccgggcat gttcgacgcc 480
gtcagcgacg gcgaactggt cgaaatcttc caggagatcg cagcctgtgg ttcagtcgtc 540
gtgggtccatg ccgagaatga aacgatcatt caagcgctcc agaagcagat caaagccgct 600
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attcagcgtg cgttactact gcagaaagaa gccggctgtc gactgattgt gcttcacgtg 720
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gatgcctcgc agttccgatc cctgcataag tacagcccggt tcgacgggat gcccgtcacg 1260
ggcgcaccgg ttctgacgat ggtgcgcgga acggtggtgg cagagaaggg agaagttctg 1320
gtcgagcagg gattcggcca gttcgtcacc cgtcacgact acgaggcgctc gaagtga 1377

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<210> 16

<211> 458

<212> PRT

<213> *Arthrobacter* sp.

<400> 16

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Met Phe Asp Val Ile Val Lys Asn Cys Arg Met Val Ser Ser Asp Gly
1           5           10           15

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Ile Thr Glu Ala Asp Ile Leu Val Lys Asp Gly Lys Val Ala Ala Ile
20           25           30

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Ser	Ser	Asp	Thr	Ser	Asp	Val	Glu	Ala	Ser	Arg	Thr	Ile	Asp	Ala	Gly			
		35					40					45						
Gly	Lys	Phe	Val	Met	Phe	Gly	Val	Val	Asp	Glu	His	Val	His	Ile	Ile			
	50					55					60							
Asp	Met	Asp	Leu	Lys	Asn	Arg	Tyr	Gly	Arg	Phe	Glu	Leu	Asp	Ser	Glu			
65					70					75					80			
Ser	Ala	Ala	Val	Gly	Gly	Ile	Thr	Thr	Ile	Ile	Glu	Met	Pro	Leu	Thr			
				85					90					95				
Phe	Pro	Pro	Thr	Thr	Thr	Leu	Asp	Ala	Phe	Leu	Glu	Lys	Lys	Lys	Gln			
			100					105					110					
Ala	Gly	Gln	Arg	Leu	Lys	Val	Asp	Phe	Ala	Leu	Tyr	Gly	Gly	Gly	Val			
		115					120					125						
Pro	Gly	Asn	Leu	Pro	Glu	Ile	Arg	Lys	Met	His	Asp	Ala	Gly	Ala	Val			
	130					135					140							
Gly	Phe	Lys	Ser	Met	Met	Ala	Ala	Ser	Val	Pro	Gly	Met	Phe	Asp	Ala			
145					150					155					160			
Val	Ser	Asp	Gly	Glu	Leu	Phe	Glu	Ile	Phe	Gln	Glu	Ile	Ala	Ala	Cys			
				165				170						175				
Gly	Ser	Val	Val	Val	Val	His	Ala	Glu	Asn	Glu	Thr	Ile	Ile	Gln	Ala			
			180					185					190					
Leu	Gln	Lys	Gln	Ile	Lys	Ala	Ala	Gly	Arg	Lys	Asp	Met	Ala	Ala	Tyr			
		195					200					205						
Glu	Ala	Ser	Gln	Pro	Val	Phe	Gln	Glu	Asn	Glu	Ala	Ile	Gln	Arg	Ala			
	210					215					220							
Leu	Leu	Leu	Gln	Lys	Glu	Ala	Gly	Cys	Arg	Leu	Ile	Val	Leu	His	Val			
225					230					235					240			

Ser Asn Pro Asp Gly Val Glu Leu Ile His Gln Ala Gln Ser Glu Gly
245 250 255

Gln Asp Val His Cys Glu Ser Gly Pro Gln Tyr Leu Asn Ile Thr Thr
260 265 270

Asp Asp Ala Glu Arg Ile Gly Pro Tyr Met Lys Val Ala Pro Pro Val
275 280 285

Arg Ser Ala Glu Met Asn Val Arg Leu Trp Glu Gln Leu Glu Asn Gly
290 295 300

Leu Ile Asp Thr Leu Gly Ser Asp His Gly Gly His Pro Val Glu Asp
305 310 315 320

Lys Glu Pro Gly Trp Lys Asp Val Trp Lys Ala Gly Asn Gly Ala Leu
325 330 335

Gly Leu Glu Thr Ser Leu Pro Met Met Leu Thr Asn Gly Val Asn Lys
340 345 350

Gly Arg Leu Ser Leu Glu Arg Leu Val Glu Val Met Cys Glu Lys Pro
355 360 365

Ala Lys Leu Phe Glu Ile Tyr Pro Gln Lys Gly Thr Leu Gln Val Gly
370 375 380

Ser Asp Ala Asp Leu Leu Ile Leu Asp Leu Asp Ile Asp Thr Lys Val
385 390 395 400

Asp Ala Ser Gln Phe Arg Ser Leu His Lys Tyr Ser Pro Phe Asp Gly
405 410 415

Met Pro Val Thr Gly Ala Pro Val Leu Thr Met Val Arg Gly Thr Val
420 425 430

Val Ala Glu Lys Gly Glu Val Leu Val Glu Gln Gly Phe Gly Gln Phe
435 440 445

Val Thr Arg His Asp Tyr Glu Ala Ser Lys
 450 455

<210> 17
 <211> 1377
 <212> DNA
 <213> *Arthrobacter* sp.

<400> 17
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 gacattcttg tgaaagacgg caaagtcgcc gcaatcagct cggacacaag tgatgttgag 120
 gcgagccgaa ccattgacgc ggggtggcaag ttcgtgatgc cgggctgtgt cgatgaacat 180
 gcgagccgaa ccattgacgc ggggtggcaag ttcgtgatgc cgggctgtgt cgatgaacat 240
 tctgcggccg tgggaggcat caccaccatc atcgagatgc cgttaacctt cccgccacc 300
 accacttttg acgccttcct cgaaaagaag aagcaggcgg ggcagcgggt gaaagttgac 360
 ttcgcgctct atggcgggtg agtgccggga aacctgccc agatccgcaa aatgcacgac 420
 gccggcgcag tgggcttcaa gtcaatgatg gcagcctcag ttccgggcat gttcgacgcc 480
 gtcagcgacg gcgaactgtt cgaaatcttc caggagatcg cagcctgtgt ttcagtcgcc 540
 gtggtccatg ccgagaatga aacgatcatt caagcgctcc agaagcagat caaagccgct 600
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gatgcctcgc agttccgatc cctgcataag tacagcccgt tcgacgggat gcccgtcacg 1260
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 gtcgagcagg gattcggcca gtctgctacc cgtcacgact acgaggcgctc gaagtga 1377

<210> 18

<211> 458

<212> PRT

<213> *Arthrobacter* sp.

<400> 18

Met Phe Asp Val Ile Val Lys Asn Cys Arg Met Val Ser Ser Asp Gly
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Ile Thr Glu Ala Asp Ile Leu Val Lys Asp Gly Lys Val Ala Ala Ile
 20 25 30

Ser Ser Asp Thr Ser Asp Val Glu Ala Ser Arg Thr Ile Asp Ala Gly
 35 40 45

Gly Lys Phe Val Met Phe Gly Val Val Asp Glu His Val His Ile Ile
 50 55 60

Asp Met Asp Leu Lys Asn Arg Tyr Gly Arg Phe Glu Leu Asp Ser Glu
 65 70 75 80

Ser Ala Ala Val Gly Gly Ile Thr Thr Ile Ile Glu Met Pro Leu Thr
 85 90 95

Phe Pro Pro Thr Thr Thr Leu Asp Ala Phe Leu Glu Lys Lys Lys Gln
 100 105 110

Ala Gly Gln Arg Leu Lys Val Asp Phe Ala Leu Tyr Gly Gly Gly Val
 115 120 125

Pro Gly Asn Leu Pro Glu Ile Arg Lys Met His Asp Ala Gly Ala Val
 130 135 140

Gly Phe Lys Ser Met Met Ala Ala Ser Val Pro Gly Met Phe Asp Ala
 145 150 155 160

Val Ser Asp Gly Glu Leu Phe Glu Ile Phe Gln Glu Ile Ala Ala Cys
 165 170 175

Gly Ser Val Ala Val Val His Ala Glu Asn Glu Thr Ile Ile Gln Ala
 180 185 190

Leu Gln Lys Gln Ile Lys Ala Ala Gly Arg Lys Asp Met Ala Ala Tyr
 195 200 205

Glu Ala Ser Gln Pro Val Phe Gln Glu Asn Glu Ala Ile Gln Arg Ala
 210 215 220

Leu Leu Leu Gln Lys Glu Ala Gly Cys Arg Leu Ile Val Leu His Val
 225 230 235 240

Ser Asn Pro Asp Gly Val Glu Leu Ile His Arg Ala Gln Ser Glu Gly
 245 250 255

Gln Asp Val His Cys Glu Ser Gly Pro Gln Tyr Leu Asn Ile Thr Thr
 260 265 270

Asp Asp Ala Glu Arg Ile Gly Pro Tyr Met Lys Val Ala Pro Pro Val
 275 280 285

Arg Ser Ala Glu Met Asn Val Arg Leu Trp Glu Gln Leu Glu Asn Gly
 290 295 300

Leu Ile Asp Thr Leu Gly Ser Asp His Gly Gly His Pro Val Glu Asp
 305 310 315 320

Lys Glu Pro Gly Trp Lys Asp Val Trp Lys Ala Gly Asn Gly Ala Leu
 325 330 335

Gly Leu Glu Thr Ser Leu Pro Met Met Leu Thr Asn Gly Val Asn Lys
 340 345 350

Gly Arg Leu Ser Leu Glu Arg Leu Val Glu Val Met Cys Glu Lys Pro
 355 360 365

Ala Lys Leu Phe Glu Ile Tyr Pro Gln Lys Gly Thr Leu Gln Val Gly
 370 375 380

Ser Asp Ala Asp Leu Leu Ile Leu Asp Leu Asp Ile Asp Thr Lys Val
 385 390 395 400

Asp Ala Ser Gln Phe Arg Ser Leu His Lys Tyr Ser Pro Phe Asp Gly
 405 410 415

Met Pro Val Thr Gly Ala Pro Val Leu Thr Met Val Arg Gly Thr Val
 420 425 430

Val Ala Glu Lys Gly Glu Val Leu Val Glu Gln Gly Phe Gly Gln Phe
 435 440 445

Val Thr Arg His Asp Tyr Glu Ala Ser Lys
 450 455

<210> 19
 <211> 1377
 <212> DNA
 <213> Arthrobacter sp.

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Ile Thr Glu Ala Asp Ile Leu Val Lys Asp Gly Lys Val Ala Ala Ile
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Ser Ser Asp Thr Ser Asp Val Glu Ala Ser Arg Thr Ile Asp Ala Gly
 35 40 45

Gly Lys Phe Val Met Phe Gly Val Val Asp Glu His Val His Ile Ile

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Ser	Ala	Ala	Val	Gly	Gly	Ile	Thr	Thr	Ile	Ile	Glu	Met	Pro	Phe	Thr	
				85					90					95		
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			100					105					110			
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		115					120					125				
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Val	Ser	Asp	Gly	Glu	Leu	Phe	Glu	Ile	Phe	Gln	Glu	Ile	Ala	Ala	Cys	
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Glu	Ala	Ser	Gln	Pro	Val	Phe	Gln	Glu	Asn	Glu	Ala	Ile	Gln	Arg	Ala	
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225					230					235					240	
Ser	Asn	Pro	Asp	Gly	Val	Glu	Leu	Ile	His	Arg	Ala	Gln	Ser	Glu	Gly	
				245					250					255		

Gln Asp Val His Cys Glu Ser Gly Pro Gln Tyr Leu Asn Ile Thr Thr
 260 265 270

Asp Asp Ala Glu Arg Ile Gly Pro Tyr Met Lys Val Ala Pro Pro Val
 275 280 285

Arg Ser Ala Glu Met Asn Val Arg Leu Trp Glu Gln Leu Glu Asn Gly
 290 295 300

Leu Ile Asp Thr Leu Gly Ser Asp His Gly Gly His Pro Val Glu Asp
 305 310 315 320

Lys Glu Pro Gly Trp Lys Asp Val Trp Lys Ala Gly Asn Gly Ala Leu
 325 330 335

Gly Leu Glu Thr Ser Leu Pro Met Met Leu Thr Asn Gly Val Asn Lys
 340 345 350

Gly Arg Leu Ser Leu Glu Arg Leu Val Glu Val Met Cys Glu Lys Pro
 355 360 365

Ala Lys Leu Phe Glu Ile Tyr Pro Gln Lys Gly Thr Leu Gln Val Gly
 370 375 380

Ser Asp Ala Asp Leu Leu Ile Leu Asp Leu Asp Ile Asp Thr Lys Val
 385 390 395 400

Asp Ala Ser Gln Phe Arg Ser Leu His Lys Tyr Ser Pro Phe Asp Gly
 405 410 415

Met Pro Val Thr Gly Ala Pro Val Leu Thr Met Val Arg Gly Thr Val
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Val Thr Arg His Asp Tyr Glu Ala Ser Lys
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